

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/559,806A

Source: IFW9

Date Processed by STIC: 4/19/06

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 04/19/2006

PATENT APPLICATION: US/10/559,806A

TIME: 13:16:35

Input Set : A:\Q91925US.APP

Output Set: N:\CRF4\04192006\J559806A.raw

```

3 <110> APPLICANT: KIM, JIN-SOO
4     SHIN, HYUN-CHUL
5     KWON, HEUNG-SUN
7 <120> TITLE OF INVENTION: TRANSDUCIBLE DNA-BINDING PROTEINS
9 <130> FILE REFERENCE: Q91925
11 <140> CURRENT APPLICATION NUMBER: 10/559,806A
12 <141> CURRENT FILING DATE: 2005-12-08
14 <150> PRIOR APPLICATION NUMBER: PCT/KR04/01385
15 <151> PRIOR FILING DATE: 2004-06-10
17 <152> PRIOR APPLICATION NUMBER: 60/477,459
18 <151> PRIOR FILING DATE: 2003-06-10
20 <160> NUMBER OF SEQ ID NOS: 72
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 11
26 <212> TYPE: PRT
27 <213> ORGANISM: Human immunodeficiency virus
29 <400> SEQUENCE: 1
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31 1           5           10
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 16
36 <212> TYPE: PRT
37 <213> ORGANISM: Drosophila melanogaster
39 <400> SEQUENCE: 2
40 Ala Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Asn
41 1           5           10           15
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 34
46 <212> TYPE: PRT
47 <213> ORGANISM: Herpes simplex virus
49 <400> SEQUENCE: 3
50 Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr
51 1           5           10           15
53 Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro
54           20           25           30
56 Val Glu
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 12
62 <212> TYPE: PRT
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

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68 <400> SEQUENCE: 4
69 Thr Ser Pro Leu Asn Ile His Asn Gly Gln Lys Leu
70 1      5      10
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 26
75 <212> TYPE: PRT
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
81 <220> FEATURE:
82 <221> NAME/KEY: MOD_RES
83 <222> LOCATION: (2)..(6)
84 <223> OTHER INFORMATION: region may encompass a range of 2-5 variable amino
85 acids
87 <220> FEATURE:
88 <221> NAME/KEY: MOD_RES
89 <222> LOCATION: (8)..(10)
90 <223> OTHER INFORMATION: variable amino acid
92 <220> FEATURE:
93 <221> NAME/KEY: MOD_RES
94 <222> LOCATION: (11)
95 <223> OTHER INFORMATION: Phe or Tyr
97 <220> FEATURE:
98 <221> NAME/KEY: MOD_RES
99 <222> LOCATION: (12)..(16)
100 <223> OTHER INFORMATION: variable amino acid
102 <220> FEATURE:
103 <221> NAME/KEY: MOD_RES
104 <222> LOCATION: (17)
105 <223> OTHER INFORMATION: hydrophobic residue
107 <220> FEATURE:
108 <221> NAME/KEY: MOD_RES
109 <222> LOCATION: (18)..(19)
110 <223> OTHER INFORMATION: variable amino acid
112 <220> FEATURE:
113 <221> NAME/KEY: MOD_RES
114 <222> LOCATION: (21)..(25)
115 <223> OTHER INFORMATION: region may encompass a range of 3-5 variable amino
116 acids
119 <400> SEQUENCE: 5
W--> 120 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
121 1      5      10      15
W--> 123 Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
124      20      25
127 <210> SEQ ID NO: 6
128 <211> LENGTH: 26
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:

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133 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
135 <220> FEATURE:
136 <221> NAME/KEY: MOD_RES
137 <222> LOCATION: (2)..(6)
138 <223> OTHER INFORMATION: region may encompass a range of 2-5 variable amino
139     acids
141 <220> FEATURE:
142 <221> NAME/KEY: MOD_RES
143 <222> LOCATION: (8)..(10)
144 <223> OTHER INFORMATION: variable amino acid
146 <220> FEATURE:
147 <221> NAME/KEY: MOD_RES
148 <222> LOCATION: (11)
149 <223> OTHER INFORMATION: variable amino acid, frequently aromatic
151 <220> FEATURE:
152 <221> NAME/KEY: MOD_RES
153 <222> LOCATION: (12)
154 <223> OTHER INFORMATION: variable amino acid
156 <220> FEATURE:
157 <221> NAME/KEY: MOD_RES
158 <222> LOCATION: (14)..
159 <223> OTHER INFORMATION: variable amino acid
161 <220> FEATURE:
162 <221> NAME/KEY: MOD_RES
163 <222> LOCATION: (17)
164 <223> OTHER INFORMATION: variable amino acid, frequently hydrophobic
166 <220> FEATURE:
167 <221> NAME/KEY: MOD_RES
168 <222> LOCATION: (18)
169 <223> OTHER INFORMATION: variable amino acid
171 <220> FEATURE:
172 <221> NAME/KEY: MOD_RES
173 <222> LOCATION: (21)..(25)
174 <223> OTHER INFORMATION: region may encompass a range of 3-5 variable amino
175     acids
177 <400> SEQUENCE: 6
W--> 178 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Glu
179     1           5           10           15
W--> 181 Xaa Xaa Arg His Xaa Xaa Xaa Xaa Xaa His
182           20           25
185 <210> SEQ ID NO: 7
186 <211> LENGTH: 260
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 7
191 Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys
192 1           5           10           15
194 Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser
195           20           25           30

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197 Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser
198      35      40      45
200 Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe
201      50      55      60
203 Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val
204 65      70      75      80
206 Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro
207      85      90      95
209 Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met
210      100      105      110
212 Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro
213      115      120      125
215 Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala
216      130      135      140
218 Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp
219 145      150      155      160
221 Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe
222      165      170      175
224 Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn
225      180      185      190
227 Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu
228      195      200      205
230 Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Ala Gln Arg Pro Pro Asp
231      210      215      220
233 Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
234 225      230      235      240
236 Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
237      245      250      255
239 Leu Leu Ser Gln
240      260
243 <210> SEQ ID NO: 8
244 <211> LENGTH: 127
245 <212> TYPE: PRT
246 <213> ORGANISM: Saccharomyces cerevisiae
248 <400> SEQUENCE: 8
249 Asn Phe Asn Gln Ser Gly Asn Ile Ala Asp Ser Ser Leu Ser Phe Thr
250 1      5      10      15
252 Phe Thr Asn Ser Ser Asn Gly Pro Asn Leu Ile Thr Thr Gln Thr Asn
253      20      25      30
255 Ser Gln Ala Leu Ser Gln Pro Ile Ala Ser Ser Asn Val His Asp Asn
256      35      40      45
258 Phe Met Asn Asn Glu Ile Thr Ala Ser Lys Ile Asp Asp Gly Asn Asn
259      50      55      60
261 Ser Lys Pro Leu Ser Pro Gly Trp Thr Asp Gln Thr Ala Tyr Asn Ala
262 65      70      75      80
264 Phe Gly Ile Thr Thr Gly Met Phe Asn Thr Thr Thr Met Asp Asp Val
265      85      90      95
267 Tyr Asn Tyr Leu Phe Asp Asp Glu Asp Thr Pro Pro Asn Pro Lys Lys
268      100      105      110

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270 Glu Ile Ser Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
271      115                      120                      125
274 <210> SEQ ID NO: 9
275 <211> LENGTH: 90
276 <212> TYPE: PRT
277 <213> ORGANISM: Saccharomyces cerevisiae
279 <400> SEQUENCE: 9
280 Asn Ser Ala Ser Ser Ser Thr Lys Leu Asp Asp Asp Leu Gly Thr Ala
281 1      5      10      15
283 Ala Ala Val Leu Ser Asn Met Arg Ser Ser Pro Tyr Arg Thr His Asp
284      20      25      30
286 Lys Pro Ile Ser Asn Val Asn Asp Met Asn Asn Thr Asn Ala Leu Gly
287      35      40      45
290 Val Pro Ala Ser Arg Pro His Ser Ser Ser Phe Pro Ser Lys Gly Val
291      50      55      60
293 Leu Arg Pro Ile Leu Leu Arg Ile His Asn Ser Glu Gln Gln Pro Ile
294 65      70      75      80
296 Phe Glu Ser Asn Asn Ser Thr Ala Cys Ile
297      85      90
300 <210> SEQ ID NO: 10
301 <211> LENGTH: 63
302 <212> TYPE: PRT
303 <213> ORGANISM: Homo sapiens
305 <400> SEQUENCE: 10
306 Val Ser Val Thr Phe Glu Asp Val Ala Val Leu Phe Thr Arg Asp Glu
307 1      5      10      15
309 Trp Lys Lys Leu Asp Leu Ser Gln Arg Ser Leu Tyr Arg Glu Val Met
310      20      25      30
312 Leu Glu Asn Tyr Ser Asn Leu Ala Ser Met Ala Gly Phe Leu Phe Thr
313      35      40      45
315 Lys Pro Lys Val Ile Ser Leu Leu Gln Gln Gly Glu Asp Pro Trp
316      50      55      60
319 <210> SEQ ID NO: 11
320 <211> LENGTH: 96
321 <212> TYPE: PRT
322 <213> ORGANISM: Homo sapiens
324 <400> SEQUENCE: 11
325 Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe Lys
326 1      5      10      15
328 Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp Thr
329      20      25      30
331 Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys Asn
332      35      40      45
334 Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu Arg
335      50      55      60
337 Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His Gln
338 65      70      75      80
340 Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser Val
341      85      90      95

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/559,806A

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Input Set : A:\Q91925US.APP  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. ~~2,3,4,5,6,8,9,10,11,12,13,14,15,16,17,18,19,21,22,23,24,25~~

Seq#:6; Xaa Pos. ~~2,3,4,5,6,8,9,10,11,12,14,17,18,21,22,23,24,25~~

**VERIFICATION SUMMARY**

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Input Set : A:\Q91925US.APP

Output Set: N:\CRF4\04192006\J559806A.raw

L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16  
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16  
L:466 M:283 W: Missing Blank Line separator, <400> field identifier  
L:595 M:283 W: Missing Blank Line separator, <400> field identifier  
L:724 M:283 W: Missing Blank Line separator, <400> field identifier  
L:853 M:283 W: Missing Blank Line separator, <400> field identifier  
L:982 M:283 W: Missing Blank Line separator, <400> field identifier